

Similarities in sequence between the dnaA homolog and sequences deposited in public sequence databases.

Sequences producing significant alignments:		Score (bits)	E Value
gi 140025 sp P06567 DNAI_BACSU PRIMOSOMAL PROTEIN DNAI	>gi 2797...	231	5e-60
gi 468268 (M15183) ORFY [Bacillus subtilis]		125	5e-28
gi 2072367 emb CAA70453 (Y09255) primosomal protein DnaI (Baci...		84	1e-15
gi 530419 emb CAA83732 (Z33058) GTP bind. CD48/PAS1/SEC18 fam...		67	2e-10
gi 2983431 (AE000713) DNA replication protein DnaC [Aquilifex aeo...		52	4e-06
gi 1176732 sp P45910 YOAM_BACSU HYPOTHETICAL 36.1 KD PROTEIN IN...		50	2e-05
gi 2127076 pir 140411 hypothetical protein 5 (xre region) - Ba...		48	1e-04
gi 1722861 sp P39782 XKDC_BACSU PHAGE-LIKE ELEMENT PBSX PROTEIN...		48	1e-04
gi 1353529 (U38906) ORF12 [Bacteriophage rlt]		46	4e-04
gi 2983000 (AE000683) chromosome replication initiator protein ...		45	8e-04
<p>>gi 140025 sp P06567 DNAI_BACSU PRIMOSOMAL PROTEIN DNAI</p> <p>>gi 279708 pir IQB544 dnaA protein homolog, 44K -</p> <p>Bacillus subtilis >gi 39881 emb CAA28633 (X04963) ORF</p> <p>311 (AA 1-311) [Bacillus subtilis]</p> <p>>gi 1769996 emb CAA99605 (Z75208) replication protein</p> <p>[Bacillus subtilis] >gi 2293281 (AF008220) DnaI</p> <p>[Bacillus subtilis] >gi 2635363 emb CAB14858 (Z99118)</p> <p>helicase loader [Bacillus subtilis]</p> <p>Length = 311</p>			
<p>Score = 231 bits (583), Expect = 5e-60</p> <p>Identities = 120/280 (42%), Positives = 177/280 (62%), Gaps = 2/280 (0%)</p>			
Query: 35	DPDVKQFLEAHRAELTNAMIDEDLNVLQEQYKQQKHVDG-HKFDPCPNFVKGHPVPELYVD 93		
	D DV+ FL+ + + MI++ LN L EY +Q K+ + +C N ++G+ P+L V+		
Sbjct: 31	QDVQAFLEKENEVIDQKMKIEKSLNKLYEYIEQSKNCSYCSDEDENNNLLEGYHPKLVVN 90		
Query: 94	NNRIKIRYLQCPCKIKYDEERFEALITSHHMORDTLNAKLKDIYMNRDRDLVMAAADD 153		
	I I Y +CP K K D+++ + L+ S ++Q-D L A + + -- RL + D		
Sbjct: 91	GRSIDIEYIECPVRRKLDQKKQCSLMKSMYIQDQLLGATFQQVDISDPSRLAMFQHVTD 150		
Query: 154	ICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIYLPEFIRTLKGGFKD 213		
	+ + KGLYLYG FG GK+F+L AIAN+L K+ S I+Y+PEF+R LK +D		
Sbjct: 151	FLKSYNETGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIVYVPEFVRELKNSLQD 210		
Query: 214	GSFEKKLHRVREANIIMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFDYSEL 273		
	+ E+KL+ V+ +LMLDDIGAE +T WVRDEVIG +L +RM +LPTFFSSNF EL		
Sbjct: 211	OTLEEKLNVMVKTTPVLMDDIGAESMTSWVRDEVIGTVLQHRMSQQLPTFFSSNFSFDEL 270		
Query: 274	EMHLAMTRDGE-EKTKAARIIEVRKSLSTPYFLSGENFRN 312		
	+HH ++ GE E- KAAR++ER+ L+ P L GEN R+		
Sbjct: 271	KHFTYSQRGEKEEVKAARLMERILYLAAPIRLDGENRRH 310		
<p>>gi 468268 (M15183) ORFY [Bacillus subtilis]</p> <p>Length = 207</p>			
<p>Score = 125 bits (310), Expect = 5e-28</p> <p>Identities = 67/190 (35%), Positives = 105/190 (55%), Gaps = 1/190 (0%)</p>			
Query: 20	DFXXXXXXXXXXNDPDVQFLEAHRAELTNAMIDEDLNVLQEQYKQQKHVDG-HKFD 78		
	DF D DV+ FL+ + + MI++ LN L EY +Q K+ + +		
Sbjct: 16	DFQNRLEQTKKVMKDDQVQAFLEKENEVIDQKMKIEKSLNKLYEYIEQSKNCSYCSDEDEN 75		
Query: 79	CPNFVKGHPVPELYVDNNRIKIRYLQCPCKIKYDEERFEALITSHHMORDTLNAKLKDIY 138		
	C N ++G+ P+L V- I I Y +CP K K D+++ + L+ S ++Q-D L A + +		
Sbjct: 76	CNNLLEGYHPKLVVNGRSIDIEYIECPVRRKLDQKKQCSLMKSMYIQDQLLGATFQQVD 135		
Query: 139	MNRDRDLVMAAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTII 198		
	++ RL + D + + KGLYLYG FG GK+F+L AIAN+L K+ S I+		
Sbjct: 136	ISDPSRLAMFQHVTDFLKSYNETGKGLYLYGKFGVGKTFMLAAIANELAEKEYSSMIV 195		
Query: 199	YLPEFIRTLK 208		
	Y+PEF+R LK		
Sbjct: 196	YVPEFVRELK 205		

002TOT"25668960

A.

SEQ ID NO:1

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121    tttttggaag cgcacgcagc tgaattaacg aatgctatga ttgatgaaga cttaaattgtg
181    ttacaagagt ataaagatca acaaaaacat tatgacggtc ataaatttgc tgattgtcca
241    aatttcgtaa aggggcatgt gcctgagtta tatgttgata ataaccgaat taaaatacgc
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361    acatctcatc atatgcaacg agatacttta aatgccaaat tgaaagatat ttatatgaat
421    catcgagacc gtcttgatgt agctatggca gcagatgata tttgtacagc aataactaat
481    ggggaacaag tgaaaggcct ttacctttat ggtccatttg ggacaggtaa atcttttatt
541    ctaggtgcaa ttgcgaatca gctcaaatct aagaaggtag gttcgacaat tatttattta
601    ccggaattta ttagaacatt aaaagggtggc tttaaagatg gttcttttga aaagaaatta
661    catcgcgtaa gagaagcaaa cattttaatg cttgatgata ttggggctga agaagtgact
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SEQ ID NO:2

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121    TSHHMQRDTL NAKLKDIYMN HRDRLDVAMA ADDICTAITN GEQVKGLYLY GPFGTGKSFI
181    LGAIANQLKS KKVRSIIYIL PEFIRTLKGG FKDGSEFEKKL HRVREANILM LDDIGAEVET
241    PWVRDEVIGP LLHYRMVHEL PTFSSNFY SELEHHLAMT RDGEEKTKAA RIIERVKSLS
301    TPYFLSGENF RNN

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Fig. 1

0958956.104200

SEQ ID NO : 3

Complete genome sequence of bacteriophage 77

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 61 tataaccccc ctcttataac cattttaagg caggtgatga aatggagatt atagtcgatg
 121 aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
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 241 attacatgtg ggaagacata aaagaaagag gtgattatga tttatttact caatctgaaa
 301 aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
 361 catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
 421 aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
 481 gtggaaacaa ggaaagataa ttttaataaa agaaagaatt gatctcttta attatctaca
 541 aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
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8581	attctgactt	aaaattaaca	ggcaacaact	tcaaataatac	cgaaaaatca	actgatagtt
8641	acaaacaaag	gattaaagaa	cttgatggaa	ctatcacagg	ttataagaaa	aacgttgatg
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8821	tacaaaaaac	atcagccgaa	tttgaagagt	tcaaaaaaagc	tcaagttgaa	gctcaaagaa
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[illegible]

Phage: Bacteriophage 77
Minimal ORF size: 33 a.a.
ORFs "with" RBS.
Number of ORFs: 99

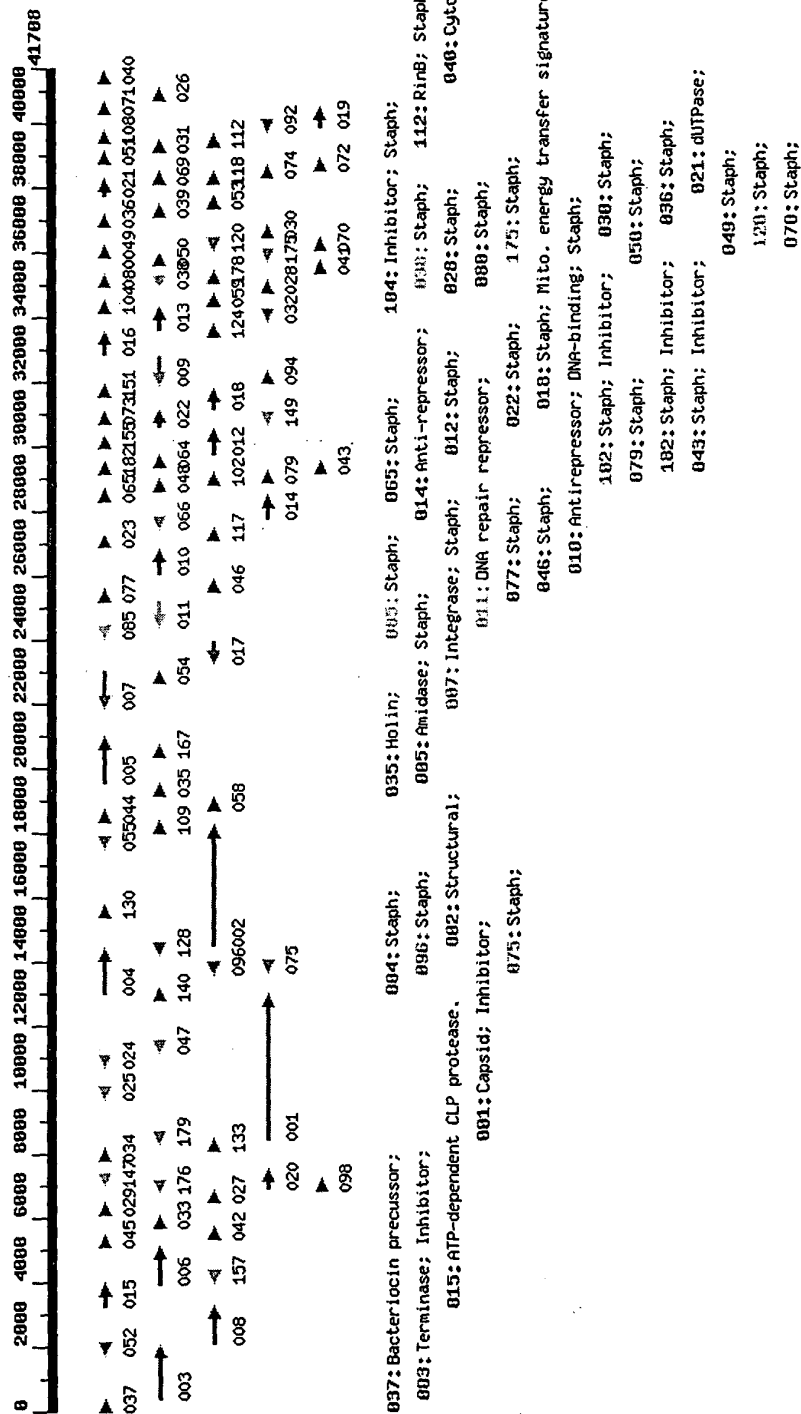


Fig. 4

P77ORF104

SEQ ID NO: 4

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61  ctcatagatg aggcacaggg cgatgaaaat aggttgtagc acctatttat ccaaaaactt
121 gcagaacgtc atacacgccc cgctatcgtc gaatattaa
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SEQ ID NO: 5

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1   MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY
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003707 25060960

Fig. 5

Predicted Tryptic Peptide Masses of Conceptual ORF in Contig 1383:

1 MGGGQSIMKqfkSIINTSQDFEKrlEKikkK 30
 31 evindpdvkQFLEAHRAeiltnamidedinv 60
 61 lqeykDQQKhdyghkFADCPNFVKghvpel 90
 91 yvdnnrIKirYLQCPCKikyDEERfeaeli 120
 121 tsnnmqrDTLNAKikDIYMNHRdrLDVAMA 150
 151 ADDICTAITNGEQVKglylygpgtgkSFI 180
 181 LGAIANQLKskKvrSTIYLPEFIRtikGG 210
 211 FKdgsfekKihrrVReanilmiddigaeet 240
 241 pwvrDEVIGPLLHYRmvhelptffssnfdy 270
 271 selehhlamtrDGEEKtkAARierVKsls 300
 301 tpyflsgenfrNN 313

Tryptic peptide fragment:

GHVPELYVDNNR

Predicted Peptide Mass MH+ = 1413.538

STIYLPEFIR

Predicted Peptide Mass MH+ = 1352.6221

SLSTPYFLSGENFR

Predicted Peptide Mass MH+ = 1618.7923

002201 25558950

A.

SEQ ID NO: 6 DnaC nucleotide *B. subtilis*

1 atgacagacc ttctgaatga cgggttcct cgcacaaata tagaagccga
 51 acaagccgtg ttaggcgcta tttttttaca gccgtctgct ttaacactgg
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 401 atgaggtcga ggatttactc agtgaagcgg aaaaaacgat tatggaagtg
 451 gcacagcgca aaaacacgag tgccttccaa aatattaagg acgtccttgt
 501 ccagacctat gataatatcg aacagcttta caatcgaaaa ggtgatataca
 551 cgggaattcc aacagggttt acggagcttg accggatgac tgcgggtttc
 601 cagcgcaacg acttgatcat tgtggctgcc cgtccttcag tagggaaaac
 651 agcctttgcc ctgaacatcg cacaaaacgt ggcgacgaag accgatgaga
 701 gcgtagcgaat tttcagtcct gagatgggtg ccgagcagct cgttatgcgt
 751 atgctctgtg ccgagggaaa tatcaatgcc cagaatctcc gtacaggtaa
 801 cctgaccgaa gaggattggg gcaagctgac gatggcaatg ggaagcctat
 851 cgaacagcgg gatttacatc gatgatacac cgggtattcg agtgagtga
 901 atccgtgcc aagtgcgcgc cttgaagcag gaaagcgggc tgggcatgat
 951 tttgatcgat tacctgcaat tgattcaggg aagcggtcgt tcaaaggaca
 1001 accgtcagca ggaagtatct gaaatttccc gtgaactgaa gtcgattgag
 1051 agggagctgc aagtccctgt tatcgcgctt tctcagcttt ccagggtgtg
 1101 tgagcagcgt caggataaac gtccgatgat gtctgatatc cgggaatcag
 1151 gaagtatcga gcaggacgcg gatattgtcg cgttccttta tcgtgatgac
 1201 tactatgaca aagaaaccga gaataaaaat attatcgaat ttattatcgc
 1251 caaacagcgt aacggcccg taggaaccgt gtctcttgag ttcgtaaaag
 1301 aatacaacaa attcgtcaac ctggaacggc gttttgatga cgcaggcggt
 1351 ccgccccggc ca

SEQ ID NO: 7 DnaC nucleotide *S. aureus*

1 ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
 51 ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
 101 CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
 151 ATTTTCCGTG CAATGATGCA CTAAATGAA GATAATAAAG AAATTGATGT
 201 TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
 251 GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
 301 AATGTTCAAT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
 351 ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
 401 TTGAAC TAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
 451 TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
 501 ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
 551 CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
 601 AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
 651 TGCGTTCGCA CTTAATATTG CACAAAAGT TGCAACGCAT GAAGATATGT
 701 ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
 751 CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
 801 TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
 851 TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
 901 GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
 951 GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
 1001 CCGATAACAG ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAGAGCA
 1051 TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG

09689952-101200

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1101 TGGTGTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151 AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201 GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251 TTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
1301 CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351 CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401 A

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dnaC nucleotide sequences alignment

Identical = 785/1413 (0.56), similar = 785/1413 (0.56)

Substitution matrix: 10 (matches), 0 (mismatches)

Gap penalty: - (50 + 3 * (gap length))

```

dnaC staph homolog   ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
dnaC B subtilis      ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
***                *      *      *      *      *      *      *      *

```

```

dnaC staph homolog   ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
dnaC B subtilis      ACAAGCCGTG TTAGGCGCTA TTTTTTACA GCCGCTGCT TTAACACTGG
***                *      *      *      *      *      *      *

```

```

dnaC staph homolog   CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
dnaC B subtilis      CTTCAGAAGT ATTGATTCCA GATGATTCT ATAGAATGTC CCACCAAAAA
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   ATTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
dnaC B subtilis      ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTG AATGAAGCGG
dnaC B subtilis      GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
dnaC B subtilis      GCGGTATTTC ATATTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   AATGTTCACT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
dnaC B subtilis      AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
dnaC B subtilis      ATTAATCAGA ACTGCAGCAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
***                *      *      *      *      *      *      *

```

```

dnaC staph homolog   TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
dnaC B subtilis      ATGAGGTCGA GGATTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
***                *      *      *      *      *      *      *

```

```

dnaC staph homolog   TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
dnaC B subtilis      GCACAGCGCA AAAACACGAG TGCCCTTCAA AATATTAAGG ACGTCCTTGT
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
dnaC B subtilis      CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
dnaC B subtilis      CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGATGAC TCGGGGTTTC
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
dnaC B subtilis      CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAA
**                *      *      *      *      *      *      *

```

```

dnaC staph homolog   TCGTTCGCGA CTTAATATTG CACAAAAAGT TGCAACGCAT GAAGATATGT
dnaC B subtilis      AGCCTTTGCC CTGAACATCG CACAAAACGT GGCGACGAAG ACCGAT---G
**                *      *      *      *      *      *      *

```

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dnaC staph homolog	ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
dnaC B subtilis	AGAGCGTAGC GATTTTCAGT CTTGAGATGG GTGCCGAGCA GCTCGTTATG
	* * * * * * * * * * * * * * * *
dnaC staph homolog	CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
dnaC B subtilis	CGTATGCTCT GTGCCGAGGG AAATATCAAT GCCCAGAATC TCCGTACAGG
	***** * * * * * * * * * * * * * *
dnaC staph homolog	TACTATGACT GAGGAAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
dnaC B subtilis	TAACCTGACC GAAGAGGATT GGGGCAAGCT GACGATGGCA ATGGGAAGCC
	* * * * * * * * * * * * * * * *
dnaC staph homolog	TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
dnaC B subtilis	TATCGAACAG CGGGATTTAC ATCGATGATA CACCGGGTAT TCGAGTGAGT
	**** * * * * * * * * * * * * * *
dnaC staph homolog	GATTTACGTT CTAATGTGCG TCGATTAAAG CAAGAACATG GCTTAGACAT
dnaC B subtilis	GAAATCCGTG CCAAGTGCCG CCGCTTGAAG CAGGAAGCGG GCGTGGGCAT
	* * * * * * * * * * * * * * * *
dnaC staph homolog	GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
dnaC B subtilis	GATTTTGATC GATTACCTGC AATTGATTCA GGAAGCGGT ---CGTTCAA
	**** * * * * * * * * * * * * * *
dnaC staph homolog	CCGATAACAG ACAACAGGAA GTTCTGAAA TCTCTCGTAC ATTAAGCA
dnaC B subtilis	AGGACAACCG TCAGCAGGAA GTATCTGAAA TTCCCGTGA ACTGAAGTCG
	* * * * * * * * * * * * * * *
dnaC staph homolog	TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG
dnaC B subtilis	ATTGCGAGGG AGCTGCAAGT CCCTGTTATC GCGCTTCTC AGCTTTCCAG
	* * * * * * * * * * * * * * *
dnaC staph homolog	TGGTGTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
dnaC B subtilis	GGGTGTTGAG CAGCGTCAGG ATAAACGTCC GATGATGTCT GATATCCGGG
	***** * * * * * * * * * * * * *
dnaC staph homolog	AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
dnaC B subtilis	AATCAGGAAG TATCGAGCAG GACGCCGATA TTGTCGCGTT CCTTTATCGT
	**** * * * * * * * * * * * * * *
dnaC staph homolog	GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
dnaC B subtilis	GATGACTACT ATGAC-----
	***** * * * * * * * * * * * *
dnaC staph homolog	TTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
dnaC B subtilis	----- AAAGAAACCG AGAATAAAAA TATTATCGAA ATTATTATCG
	* * * * * * * * * * * * * * *
dnaC staph homolog	CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
dnaC B subtilis	CCAAACAGCG TAACGGCCCG GTAGGAACCG TGTCTCTTGC GTTCGTAAAA
	* * * * * * * * * * * * * * *
dnaC staph homolog	CAATATAATA AATTTACCGA ----- --TATCGATT ATGCACATGC
dnaC B subtilis	GAATACAACA AATTCGTCAA CCTGGAACCG CGTTTGTATG ACGCAGGCGT
	***** * * * * * * * * * * * *
dnaC staph homolog	AGATATGATG TAA
dnaC B subtilis	TCCGCCCGGC GCA
	*

1	MTDLLNDRLP	PQNIEAEQAV	LGAIFLQPSA	LTLASEVLIP	DDFYRMSSHQK
51	IYNAMLVLGD	RGEVDLVTV	TSELANTDLL	EEVGGISYLT	DIANSVPTAA
101	NIEYYAKIVE	EKSILRRLIR	TATTIAQDGY	TREDEVEDLL	SEAEKTIMEV
151	AQRKNTSAFQ	NIKDVLVQTY	DNIEQLYNRK	GDITGIPTGF	TELDRMTAGF
201	QRNDLIIVAA	RPSVGKTAF	LNIAQNVATK	TDESVAIFSL	EMGAEQLVMR
251	MLCAEGNINA	QNLRTGNLTE	EDWGKLTAM	GSLNSNGIYI	DDTPGIRVSE
301	IRAKCRRLKQ	ESGLGMILID	YLQLIQGSGR	SKDNRQQEVS	EISRELKSIA
351	RELQVPVIAL	SQLSRGVEQR	QDKRPMMSDI	RESGSIEQDA	DIVAFLYRDD
401	YDKEKETENKN	IIEIIIAKQR	NGPVGTVSLA	FVKEYNKFVN	LERRFDDAGV
451	PPGA				

1	MDRMYEQNQM	PHNNEAEQSV	LGSIIIDPEL	INTTQEVLLP	ESFYRGAHQH
51	IFRAMMHLNE	DNKEIDVVTL	MDQLSTEGTL	NEAGGPQYLA	ELSTNVPTTR
101	NVQYYTDIVS	KHALKRRLIQ	TADSIANDGY	NDELELDAIL	SDAERRILEL
151	SSSRESDGFK	DIRDVLGQVY	ETAEELDQNS	GQTPGIPTGY	RDLDQMTAGF
201	NRNDLIILAA	RPSVGKTAF	LNIAQKVATH	EDMYTVGIFS	LEMGADQLAT
251	RMICSSGNVD	SNRLRTGTMT	EEDWSRFTIA	VGKLSRTKIF	IDDTPGIRIN
301	DLRSKCRRLK	QEHGLDMIVI	DYLQLIQSGS	SRASDNRQQE	VSEISRTLKA
351	LARELECPVI	ALSQLSRGVE	QRQDKRPMMS	DIRESGSIEQ	DADIVAFLYR
401	DDYYNRGGDE	DDDDGGGFEP	QTNDENGEIE	IIIAKQRNGP	TGTVKLHFMK
451	QYNKFTDIDY	AHADMM			

Identical = 265/471 (0.56), similar = 345/471 (0.73)
Substitution matrix: blosum62
Gap penalty: - (11 + 1 * (gap length))

dnaC Staph homolog	MDRMYEQNQM	PHNNEAEQSV	LSGIIDPEL	INTTQEVLLP	ESFYRGAHQH
dnaC B subtilis	MTDLLNDRLP	PQNIEAEQAV	LGAIFLQPSA	LTLLASEVLIP	DDFYRMSHQK
	* +	* * ****+	***+ + *	+ ****+	+ *** +**
dnaC Staph homolog	IFRAMMHLNE	DNKEIDVVTL	MDQLSTEGTL	NEAGGPQYLA	ELSTNVPTTR
dnaC B subtilis	IYNAMLVLGD	RGEPVDLVTV	TSELANTDLL	EEVGGISYLT	DIANSVPTAA
	*+ ** * +	+ ++++++	+* * *	* ** **	+++ ****
dnaC Staph homolog	NVQYYTDIVS	KHALKRRLIQ	TADSIANDGY	NDELELDAIL	SDAERRILEL
dnaC B subtilis	NIEYYAKIVE	EKSILRRLIR	TATTIAQDGY	TREDEVEDLL	SEAEKTIMEV
	*++** **	+ ++ ****+	** +** **	* **++ +*	*++++ *++
dnaC Staph homolog	SSSRESDGFK	DIRDVLGVQY	ETAELDQNS	GQTPGIPTGY	RDLQMQTAGF
dnaC B subtilis	AQRKNTSAFQ	NIKDVLVQTY	DNIEQLYNRK	GDITGIPTGF	TELDRLMTAGF
	+ + + **	+***** * *	+ **	* *****	+*****
dnaC Staph homolog	NRNDLIILAA	RPSVGKTAFA	LNIAQKVATH	EDMYTVGIFS	LEMGAQLAT
dnaC B subtilis	QRNDLIIVAA	RPSVGKTAFA	LNIAQNVATK	TD-ESVAIFS	LEMGAQLVM
	*****+**	*****	***** **	* +* **	*****+**
dnaC Staph homolog	RMICSSGNVD	SNRLRTGTMT	EEDWSRFTIA	VGKLSRTKIF	IDDTPGIRIN
dnaC B subtilis	RMLCAEGNIN	AQNLRGTGNLT	EEDWGKLTMA	MGSLNSNGIY	IDDTPGIRVS
	+* *	+ ****	***+ + **	+* ** + *	***+****

dnaC Staph homolog
dnaC B subtilis

DLRSKCRLK QEHGLDMIVI DYQLIQSG SRASDNRQE VSEISRTLKA
EIRAKCRLK QESGLGMILI DYQLIQSG -RSKDNRQE VSEISRELKS
++++***** ** ** **+ ***** **+ ***** **+

dnaC Staph homolog
dnaC B subtilis

LARELECPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
IARELQVPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
+*****+ *** ***** ***** ***** *****

dnaC Staph homolog
dnaC B subtilis

DDYYNRGDE DDDDDGGFEP QTNDENGEIE IIIAKQRNGP TGTVKLHFMK
DDYYDK---- ----- ETENKN-IIIE IIIAKQRNGP VGTVSLAFVK
++++*+ **++* ** ***** ** * **+

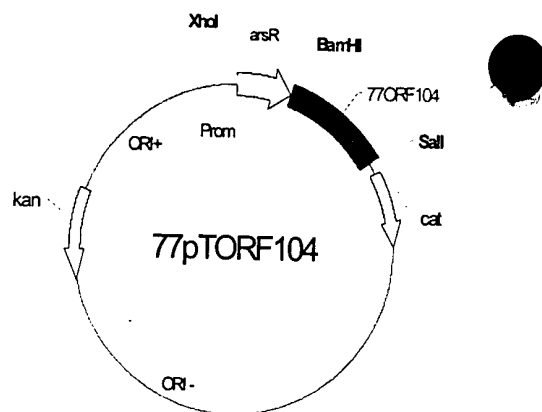
dnaC Staph homolog
dnaC B subtilis

QYNKFTDIDY AHADM----- M
EYNKFVNLER RFDDAGVPPG A
*****++* *

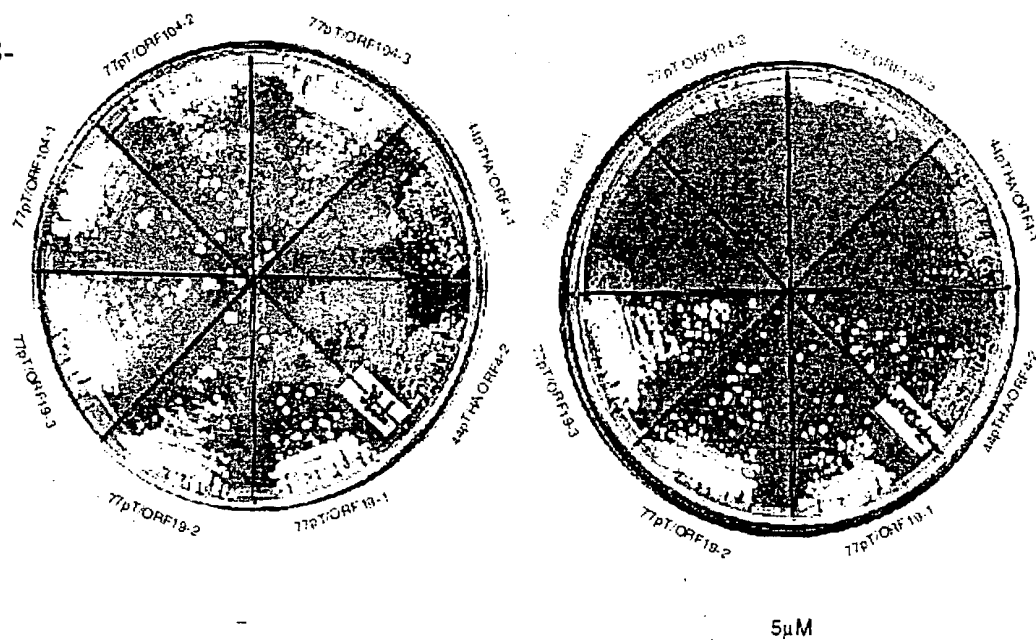
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FIGURE 7

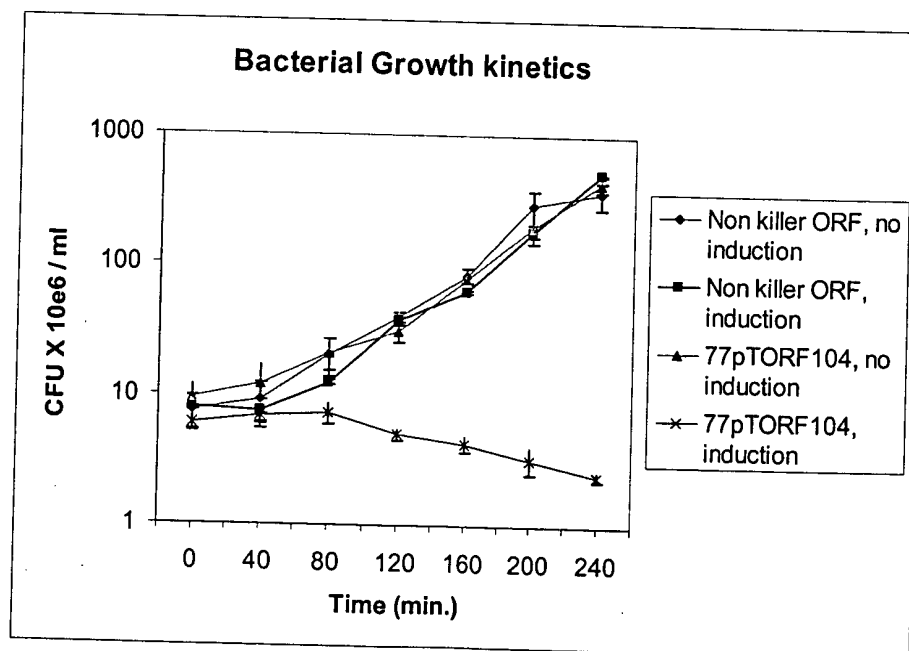
A-



B-



C-



GST

GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0

ACB 0 0.1 0.5 1.0 2.0 Mr

002101"25668960

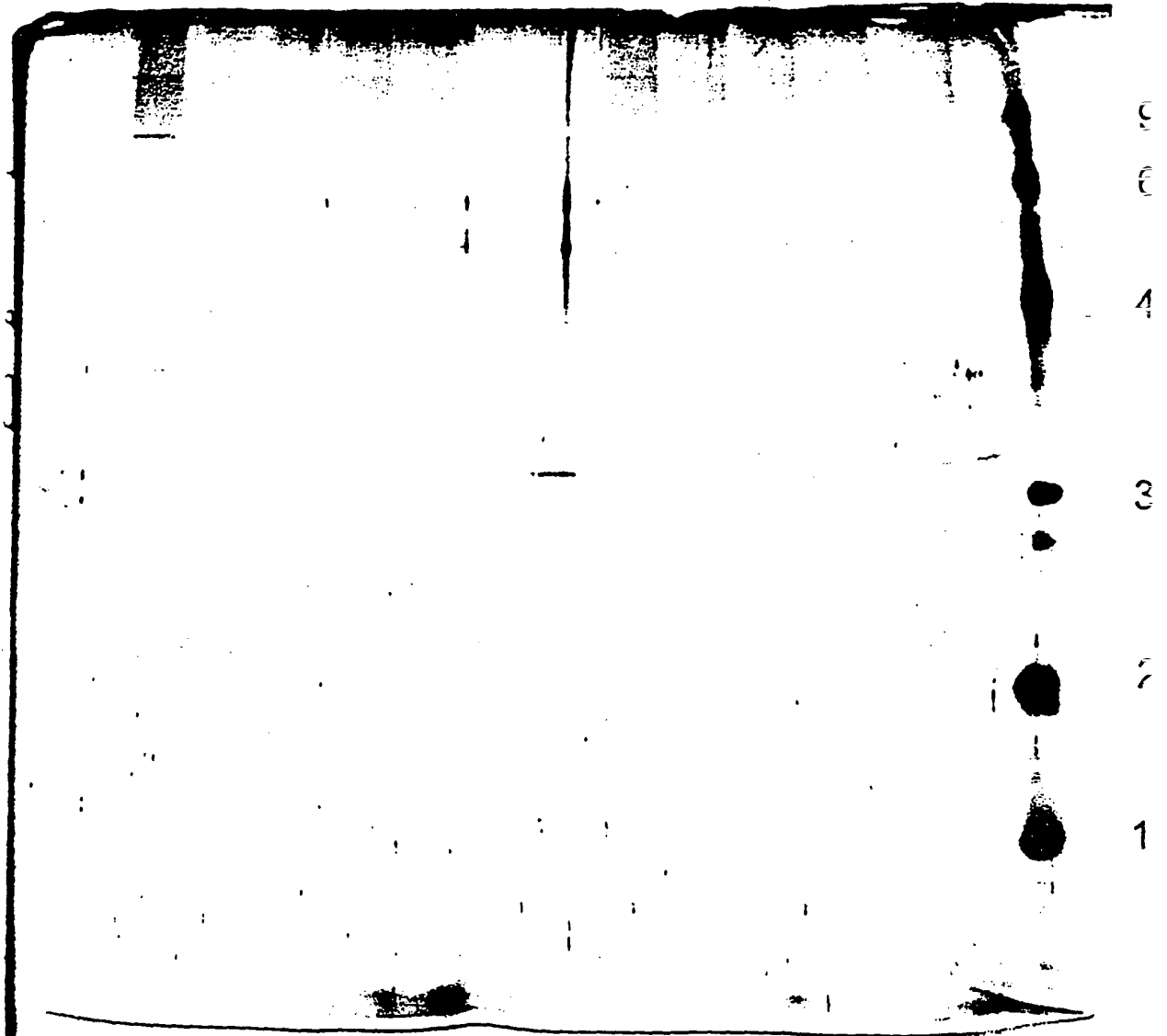


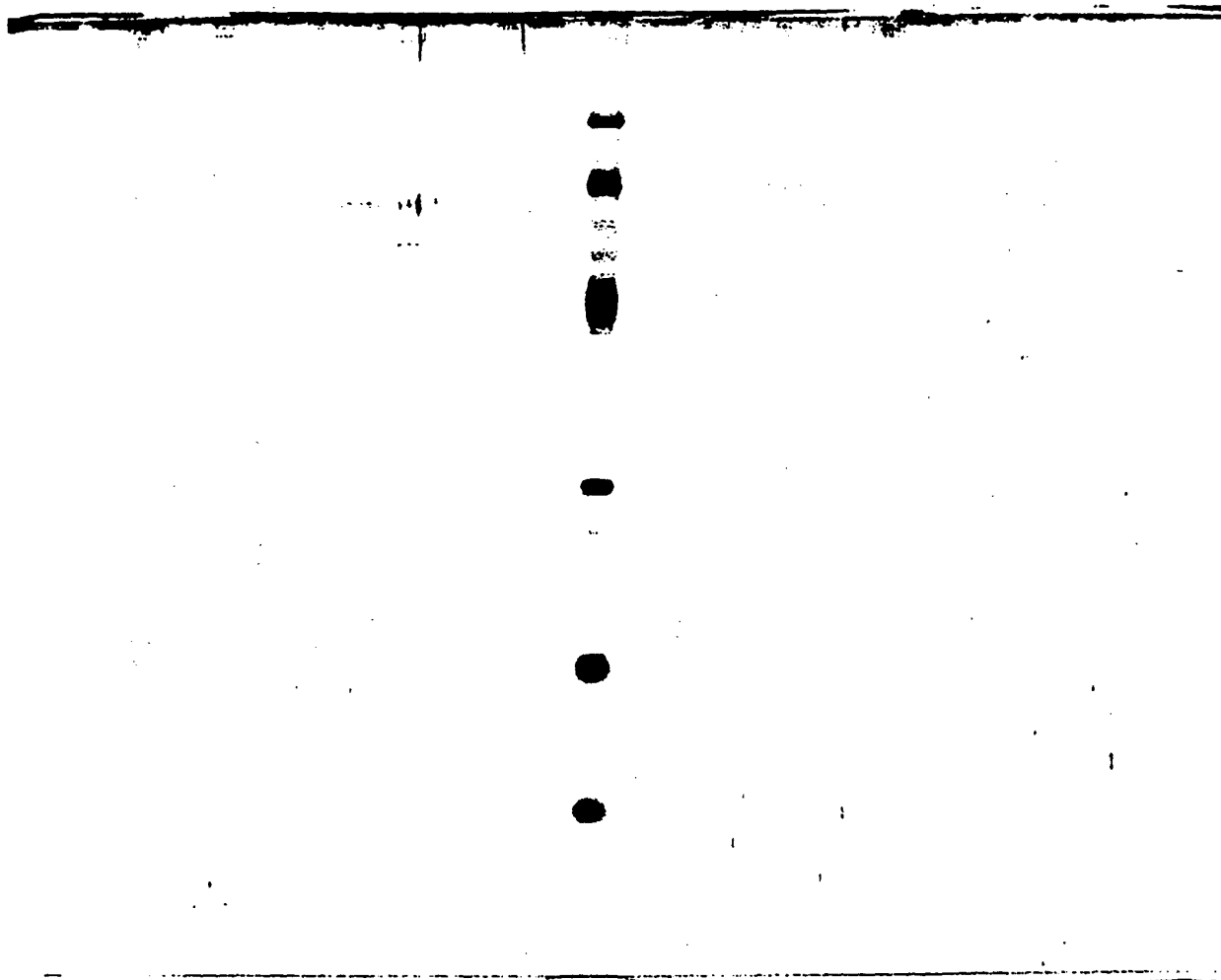
Fig. 8 A

GST

GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0 Mr

ACB 0 0.1 0.5 1.0 2.0



002101" 25668960

8B

GST

GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0 ACB 0 0.1 0.5 1.0 2.0

97

66

45

30

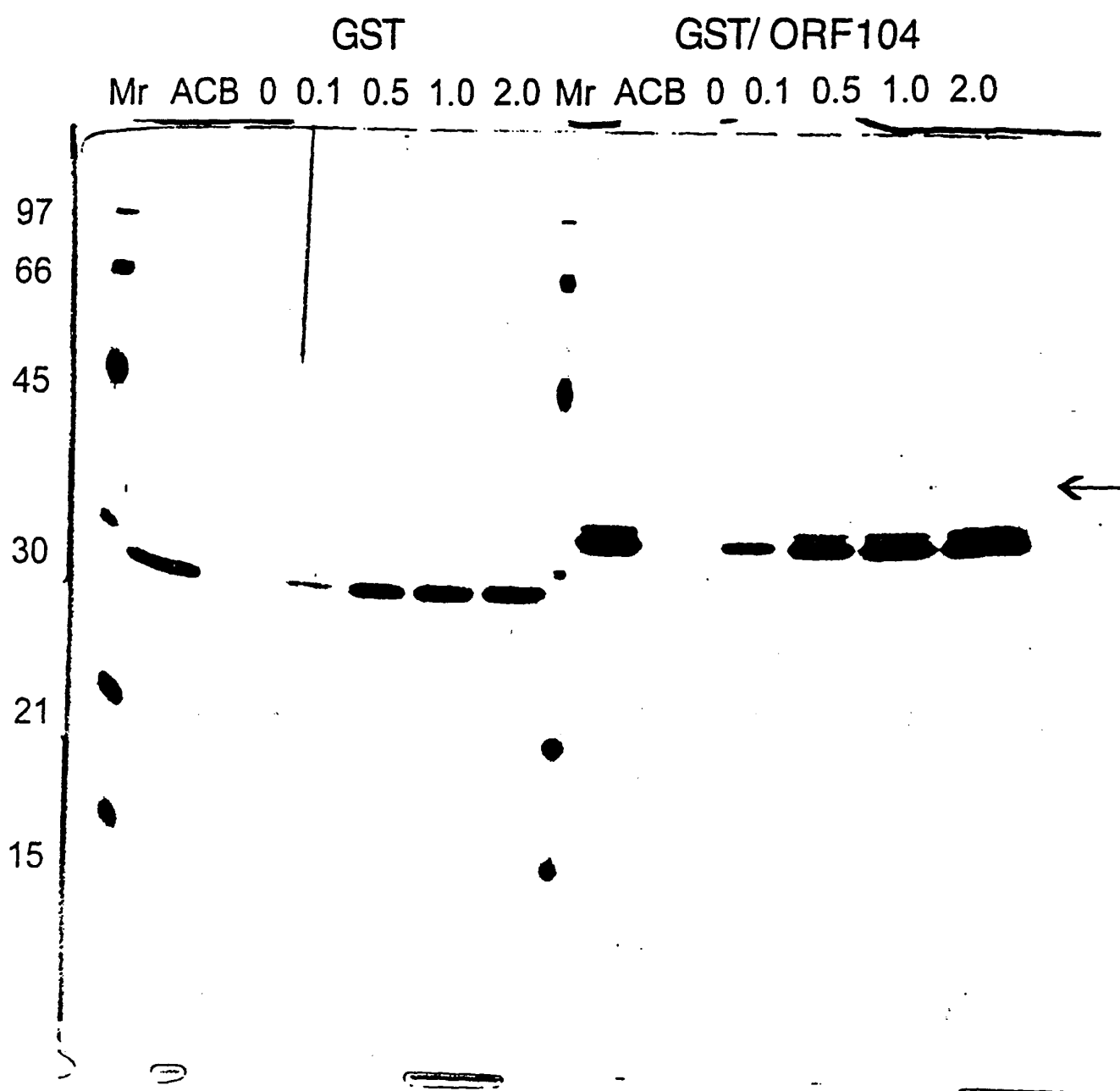
21

15

09689952-101200

8C

002101" 25668960



8D

0966962-10100

GST :						GST/ ORF104						C	L	
ACB	0	0.1	0.5	1.0	2.0	Mr	ACB	0	0.1	0.5	1.0	2.0	2.0	2.0

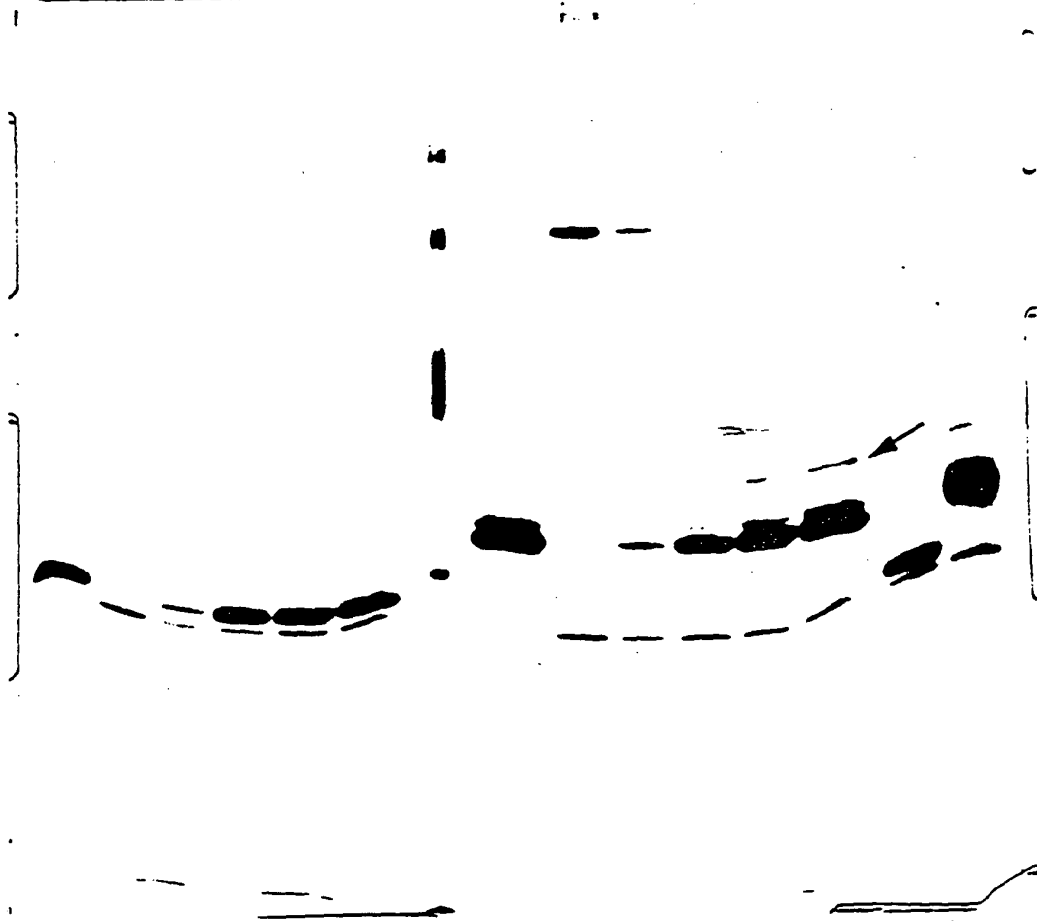


Fig. 9

002TOT 2568960

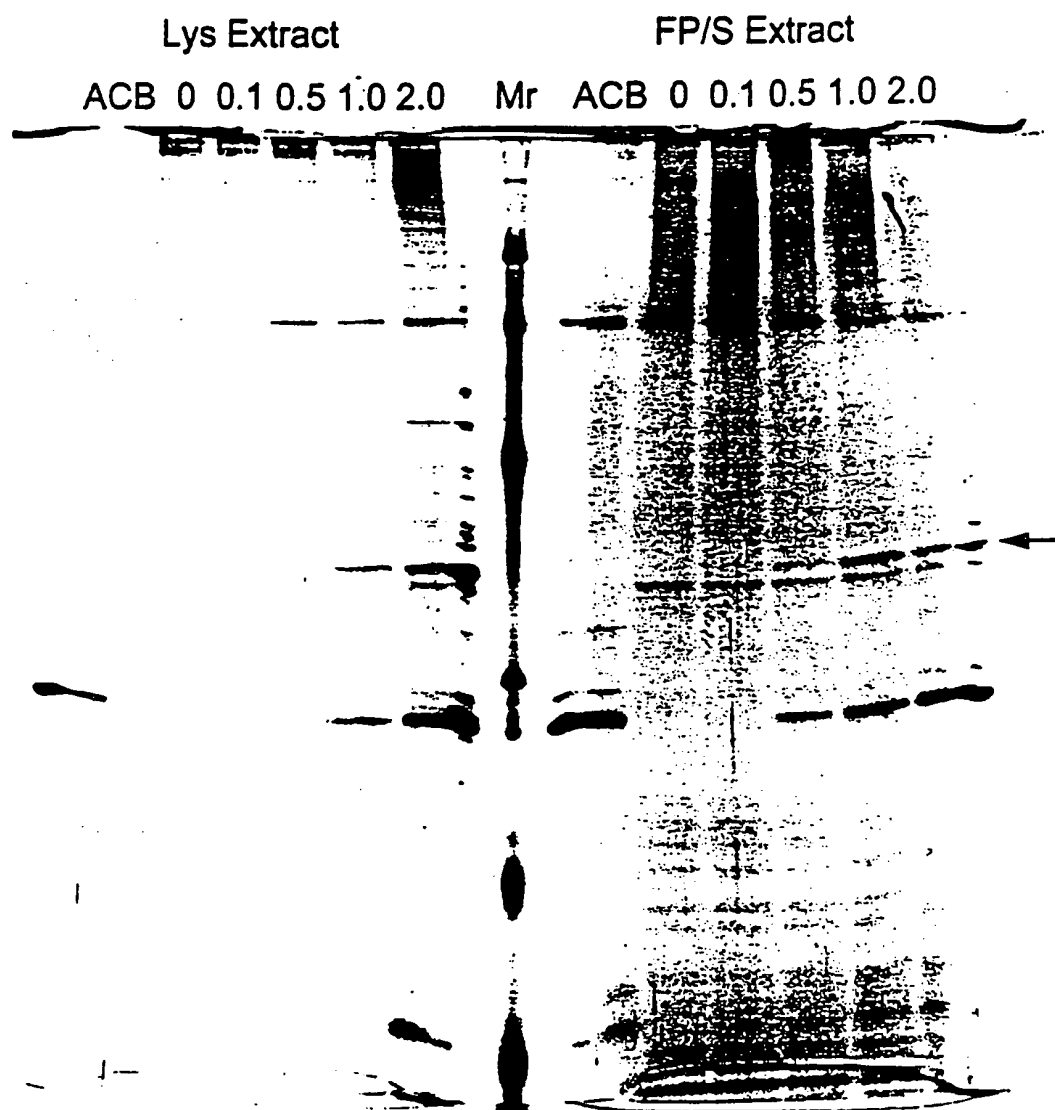
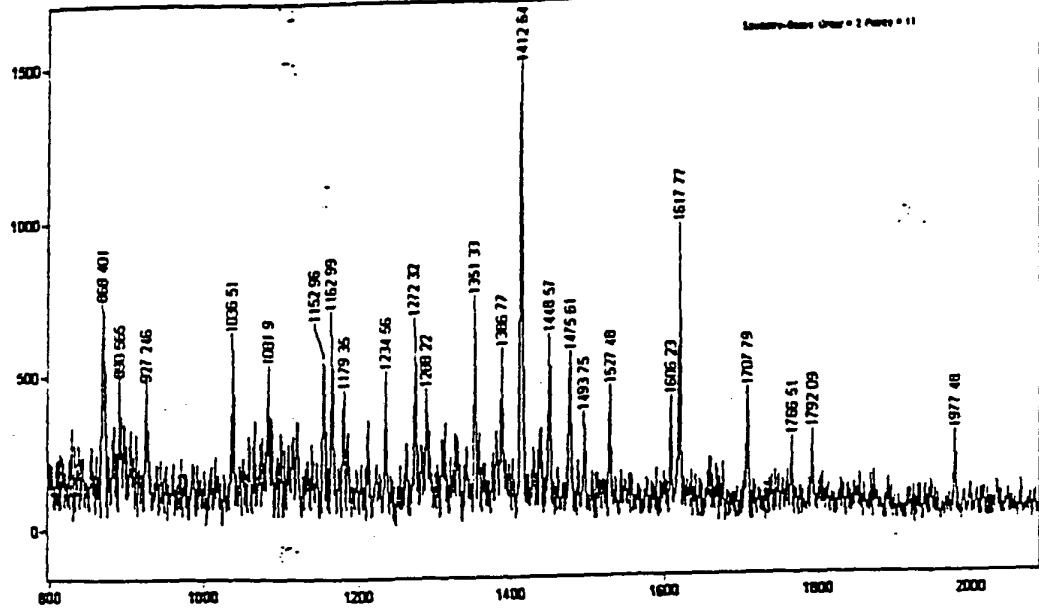


Fig. 10

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Cable Wire Voltage: 0.070 V
Duty: 170.0 Hz
Spectrum: 16
Unit: 1000
Scan: 1000
Pressure: 3.21e-03
Low Mass Gate: OFF
Tune on Scanner: 30.0 OFF
Negative Ion: OFF
Collision: 60.00 V.02 MS



ii) Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

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This File # 1: C:\BIOREAL\DATA\7-1\SMOOTH.MS
Comment: Page 525 1

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Scan: 1000
Acquiring Voltage: 2000
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Duty: 170.0 Hz
Spectrum: 16
Unit: 1000
Scan: 1000
Pressure: 3.21e-03
Low Mass Gate: OFF
Tune on Scanner: 30.0 OFF
Negative Ion: OFF
Collision: 60.00 V.02 MS

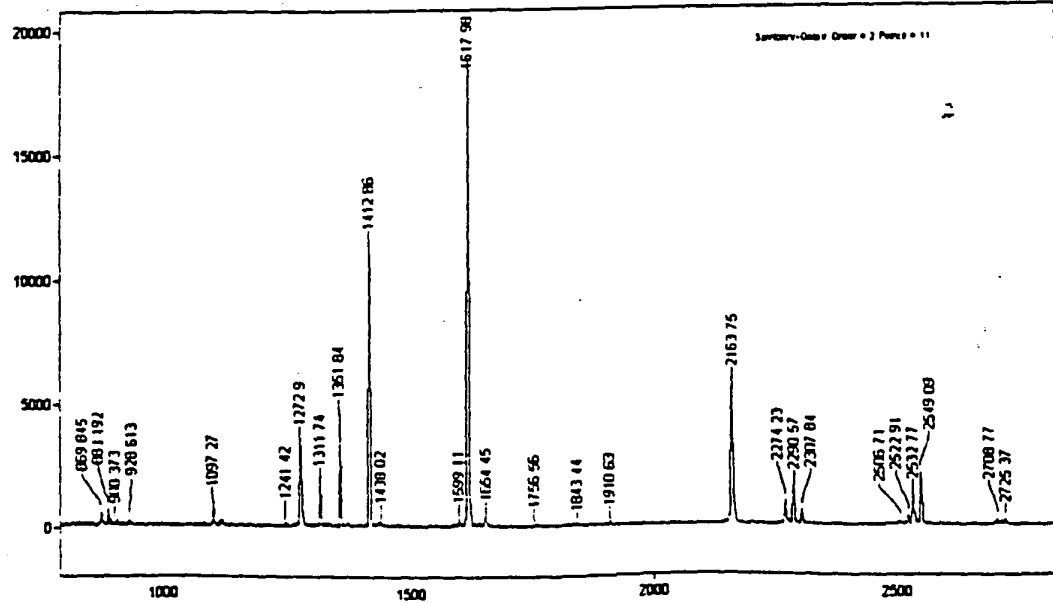
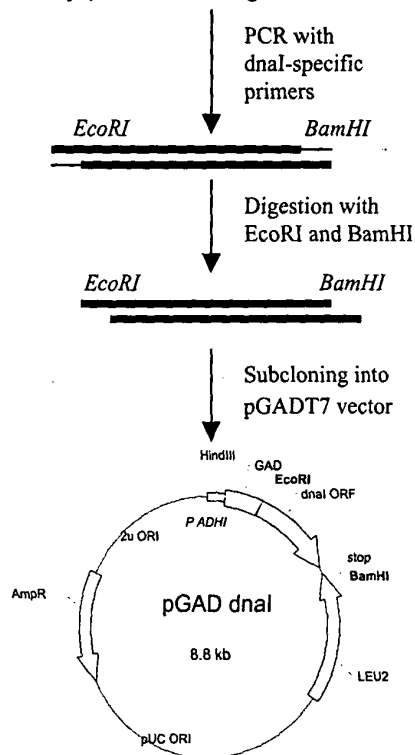
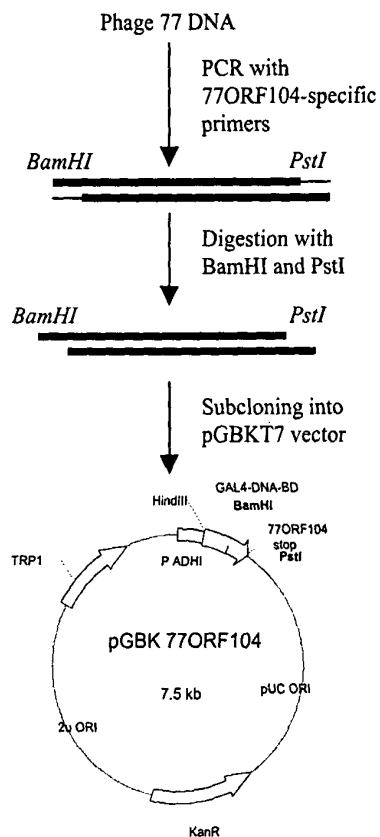


Fig. 11

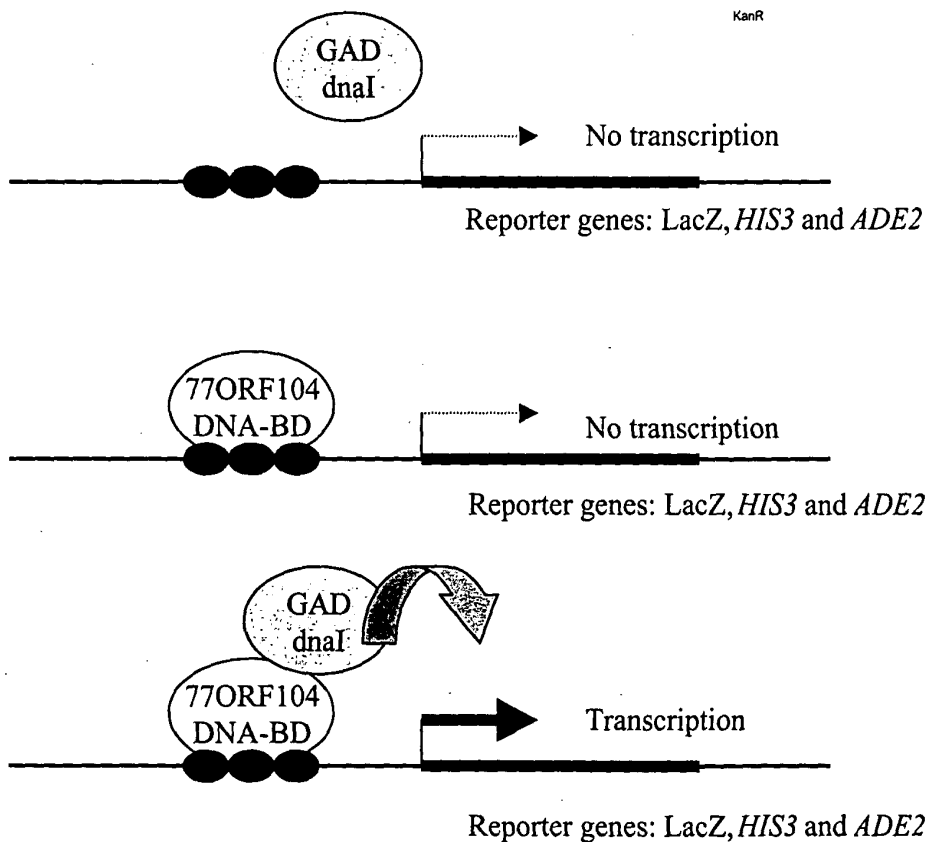
A- *Staphylococcus aureus* genomic DNA



B-



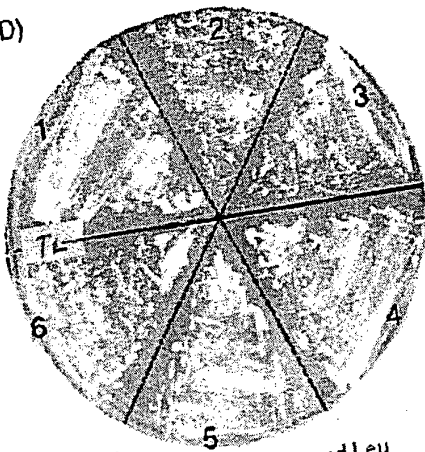
C-



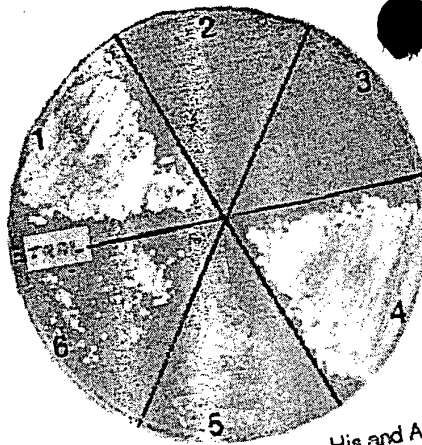
002107-25668960

Fig. 12 D + e

D)



SD plate without Trp and Leu

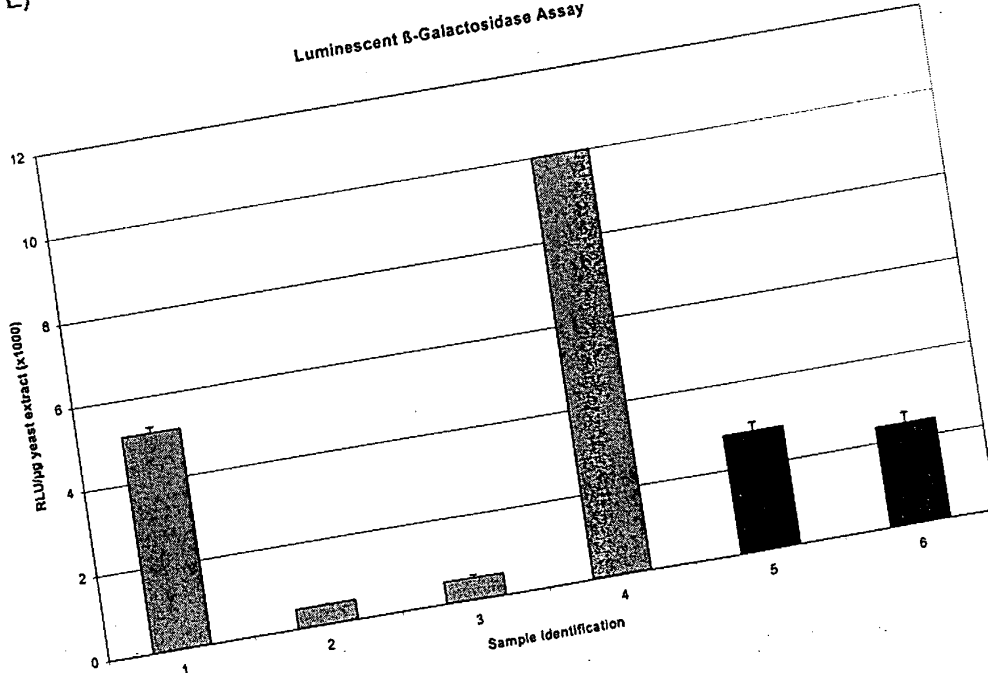


SD plate without Trp, Leu, His and Ade

- 1) pGBKT7-53 and pGADT7-T
- 2) pGBKT7-53 and pGAD dna I
- 3) pGBKT7-ORF104 and pGADT7-T
- 4) pGBKT7-LAM and pCL1
- 5) pGBKT7-ORF104 and pGAD dna I
- 6) pGBKT7-ORF104 and pGADT7-ORF104

E)

Luminescent β -Galactosidase Assay



002101 2565950

Effect of 77ORF 104 expression on 3H-Thymidine incorporation

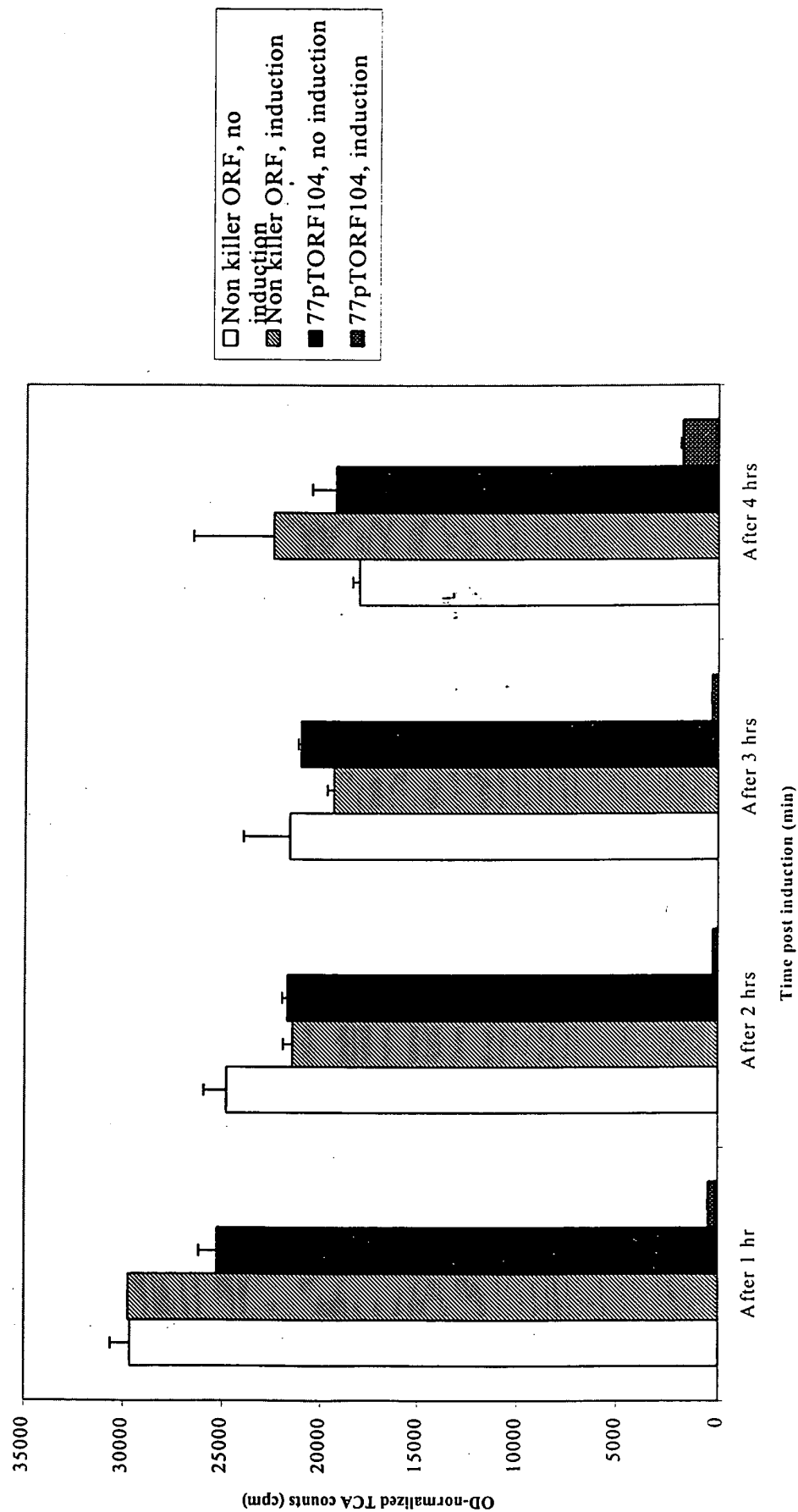
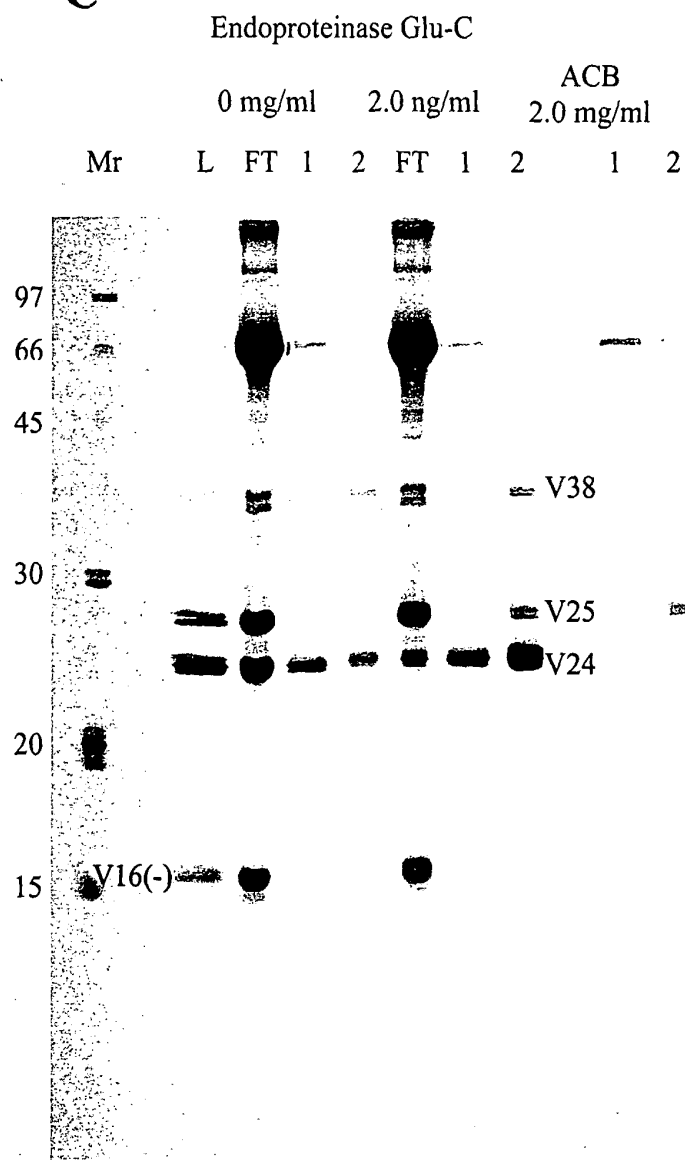


FIGURE 14A

C



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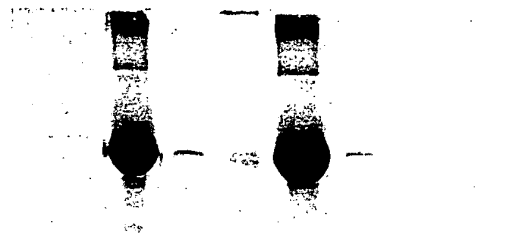
URE 14B

Chymotrypsin

0 mg/ml

2.0 ng/ml

L FT 1 2 FT 1 2



C38

C25
C24
C23
C22
C21
C20

C16(-)
C15(-)

C14

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FIGURE 14C

Amino acid residues corresponding to interacting partial proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO: 2 fragment interacting with 77ORF104	
		from amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313
SEQ ID NO: 2	Complete	1	313

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FIGURE 15

SEQ ID NO: 16

>*S.aureus* dnaI : amino acid 150-313

AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPFIRTLKG
GFKDGSFEKKLHRVREANILMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD
YSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYFLSGENFRNN

SEQ ID NO: 17

>*S.aureus* dnaI : nucleotide 448-942

gcagcagatgatattgtacagcaataactaatggggaacaagtgaaggcctttacctt
tatgggtccatttgggacaggtaaatcttttattctaggtgcaattgcgaatcagctcaaa
tctaagaagggtacgttcgacaattatttattaccggaatttattagaacattaaaagg
ggctttaagatggttcttttgaagaaattacatcgcgtaagagaagcaaacatttta
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggtaattgga
cctttgctacattatcgaatggttcatgaattaccaacattctttagttctaattttgac
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca
gcacgtattattgaacgtgtcaaatctttgtcaacaccatactttttatcaggagaaaat
ttcagaacaattga

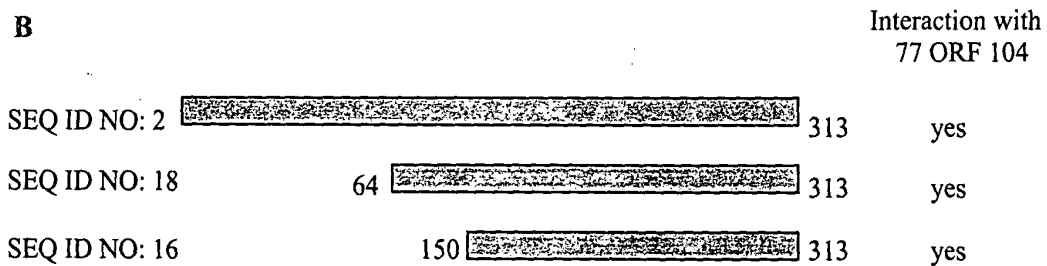
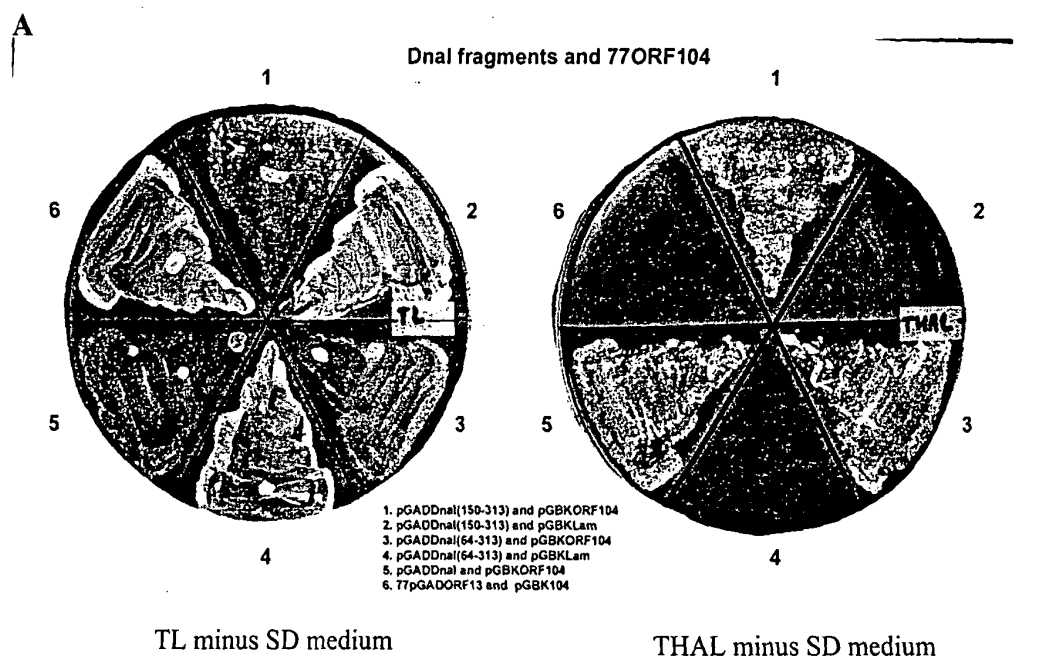
SEQ ID NO: 18

>*S.aureus* dnaI : amino acid 64-313

YKDQQKHVDGHKFAADCPNFVKGHPVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHH
MQRDTLNAKLKDIYMNHRDLVDVMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAI
ANQLKSKKVRSTIIYLPFIRTLKGGFKDGSFEKKLHRVREANILMLDDIGAEVTPWVR
DEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYF
LSGENFRNN

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FIGURE 16



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